

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 4, 2005, 12:03:24 ; Search time 189 Seconds
(without alignments)
809.787 Million cell updates/sec

Title: US-10-006-867-2

Perfect score: 1392

Sequence: 1 MMWFOGSLFSLFSAVIMTS.....YDTAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

'UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1392	100.0	266	2 Q6UX65	Q6UX65 homo sapien
2	1392	100.0	266	2 AaQ88856	AaQ88856 homo sapi
3	1245	89.4	267	2 Q9CR48	Q9CR48 m mus muscu
4	1235	88.7	267	2 Q9D520	Q9D520 mus muscu
5	1078	77.4	208	2 Q86VD3	Q86VD3 homo sapien
6	805.5	57.9	180	2 Q9DB35	Q9DB35 mus muscu
7	764.5	54.9	272	2 Q6IQ10	Q6IQ10 brachydanio
8	764.5	54.9	272	2 AAH71426	AAH71426 brachydan
9	725	52.1	136	2 Q8NBQ4	Q8NBQ4 homo sapien
10	492.5	35.4	238	2 Q8N82	Q8N82 homo sapien
11	479.5	34.4	238	2 Q9DC58	Q9DC58 mus muscu
12	479.5	34.4	238	2 BAB23366	BAB23366 mus muscu
13	471.5	33.9	287	2 Q6NRS6	Q6NRS6 xenopus lae
14	471.5	33.9	287	2 AAH70646	AAH70646 xenopus l
15	439.5	31.6	238	2 Q8QCB2	Q8QCB2 oncorhynch
16	388.5	27.9	282	2 Q7Q861	Q7Q861 anopheles g
17	361.5	26.0	246	2 Q77262	Q77262 drosophila
18	318.5	22.9	252	2 Q86F93	Q86F93 schistosoma
19	288	20.7	271	2 Q93319	Q93319 caenorhabdi
20	262	18.8	238	2 Q8R218	Q8R218 mus muscu
21	251.5	18.1	181	2 Q6XHP5	Q6XHP5 drosophila
22	251.5	18.1	181	2 AAR10251	AAR10251 drosophi
23	251	18.0	132	2 Q9NUN1	Q9NUN1 homo sapien
24	251	18.0	132	2 AAH13773	AAH13773 homo sapi
25	240	17.2	132	2 Q78J26	Q78J26 mus muscu
26	203	14.6	249	2 Q8C8S3	Q8C8S3 mus muscu
27	201.5	14.5	271	2 Q6GPL4	Q6GPL4 xenopus lae
28	191.5	13.8	257	2 Q6IQJ3	Q6IQJ3 brachydanio
29	191.5	13.8	257	2 AAH71413	AAH71413 brachydan
30	185.5	13.3	219	2 Q6P6P1	Q6P6P1 mus muscu
31	185.5	13.3	219	2 AAH62109	AAH62109 mus muscu

32	183.5	13.2	294	2 Q7SXX4	Q7SXX4 brachydanio
33	172.5	12.4	243	2 Q86IK0	Q86IK0 dictyosteli
34	161.5	11.6	123	2 Q8C9L9	Q8C9L9 mus muscu
35	160.5	11.5	271	2 Q86TGL	Q86TGL homo sapien
36	157.5	11.3	271	2 Q9QZB9	Q9QZB9 rattus norv
37	157.5	11.3	271	2 AAH72517	AAH72517 rattus no
38	151.5	10.9	271	2 Q91WN2	Q91WN2 mus muscu
39	150.5	10.8	243	2 Q86K17	Q86K17 dictyosteli
40	120	8.6	224	2 Q23135	Q23135 caenorhabdi
41	112.5	8.1	252	2 Q9U3J7	Q9U3J7 caenorhabdi
42	112.5	8.1	252	2 CAB62801	CAB62801 caenorhab
43	106.5	7.7	140	2 Q8K117	Q8K117 mus muscu
44	103	7.4	299	2 Q6CDS5	Q6CDS5 yarrowia li
45	103	7.4	332	1 HMEC_ARCFU	O29749 archaeoglob

ALIGNMENTS

RESULT 1

Q6UX65	PRELIMINARY;	PRT;	266 AA.
AC	Q6UX65		
DT	05-JUL-2004 (Tremblrel. 27, Created)		
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)		
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)		
DE	WPQ154.		
GN	ORFName=UNQ154;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
NCBI	TaxID=9606;		
[1]	SEQUENCE FROM N.A.		
RP	MEDLINE=22887296; PubMed=12975309;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brub J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Haldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment.";		
RL	Genome Res. 13:2265-2270(2003).		
DR	EMBL; AY358492; AAQ8856.1; -.		
SQ	SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;		

Query Match	100.0%;	Score 1392;	DB 2;	Length 266;
Best Local Similarity	100.0%;	Pred. No. 5.7e-108;		
Matches 266;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MMWFOGSLFSLFSAVIMTSAAPIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML	60	
DB	1	MMWFOGSLFSLFSAVIMTSAAPIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML	60	
QY	61	NIAAVLCIATIIYVRYKQVHALSPERNVIKLNKAGLVGLISCLGLSIVANFQKTLFPA	120	
DB	61	NIAAVLCIATIIYVRYKQVHALSPERNVIKLNKAGLVGLISCLGLSIVANFQKTLFPA	120	
QY	121	HVSGAVLTFGMSLYMFVQTILSYOMPKIHQKQVFWIRLLIVICGVSALSMTCSSVL	180	
DB	121	HVSGAVLTFGMSLYMFVQTILSYOMPKIHQKQVFWIRLLIVICGVSALSMTCSSVL	180	
QY	181	HSGNFGTDLQKLNWNPDKGYVLHMTTAAWSMSFSFPGFLLTYRDFQKISLRVAN	240	
DB	181	HSGNFGTDLQKLNWNPDKGYVLHMTTAAWSMSFSFPGFLLTYRDFQKISLRVAN	240	
QY	241	LHGLTYDTPACPINNERTRLSRDI	266	

```
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266
RESULT 2
AAQ88856
ID AAQ88856 PRELIMINARY; PRT; 266 AA.
AC AAQ88856;
DT 02-MAR-2004 (TEMBLrel. 27, Created)
DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
DE WPFQ154.
GN UNQ154.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brueh J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AX358492; AAQ88856.1; -
SQ SEQUENCE 266 AA; 2766 MW; 4F91D5C212D458E5 CRC64;
Query Match 100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.7e-108;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MWFFQGLSPALSVITWTSAAPIFYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWFFQGLSPALSVITWTSAAPIFYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLCIATIVYRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFQKTLFPA 120
Db 61 NIAAVLCIATIVYRYKQVHALSPENVIKLNKAGLVGLISCLGLSIVANFQKTLFPA 120
QY 121 HVGSAVLTFMGSLYMFVQTLISYQMPKIHGQVFWIRLLLVWCGVSALSMTCSSYL 180
Db 121 HVGSAVLTFMGSLYMFVQTLISYQMPKIHGQVFWIRLLLVWCGVSALSMTCSSYL 180
QY 181 HSGNFGTDLEQKLNWPKDGYVLHMTTAAEWSMSFSPFGFLTVIRDFQKISLRVEAN 240
Db 181 HSGNFGTDLEQKLNWPKDGYVLHMTTAAEWSMSFSPFGFLTVIRDFQKISLRVEAN 240
QY 241 LHGLTLYDTAPCPINNERTLLSRDI 266
Db 241 LHGLTLYDTAPCPINNERTLLSRDI 266
RESULT 3
Q9CR48
ID Q9CR48 PRELIMINARY; PRT; 267 AA.
AC Q9CR48;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE insert library, clone:261031818 product:hypothetical protein, full
DE length enriched library, (Mus musculus adult male tongue cDNA, RIKEN full-
DE length enriched library, clone:2310056E01 product:hypothetical
DE protein, full insert sequence) (Mus musculus 10 days lactation, adult
DE female mammary gland cDNA, RIKEN full-length enriched library,
```

```
DE clone:D730039I03 product:hypothetical protein, full insert
DE sequence).
GN Name=2610318G18R1K;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RC MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RC MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RA The PANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RC MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RC MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RN [6]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Tongue, and Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
```



```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AK008532; BAB25725.1; -.
DR ENBL; BC024458; AAH24458.1; -.
DR MGD; MGI:1919359; 2010305N14rik.
KW Hypothetical protein.
SQ SEQUENCE 180 AA; 20324 MW; 7952C2302D9235DF CRC64;

Query Match 57.9%; Score 805.5; DB 2; Length 180;
Best Local Similarity 60.0%; Pred. No. 3e-59;
Matches 159; Conservative 12; Mismatches 7; Indels 87; Gaps 1;

QY 1 MWMFOGSLPLPSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWMFOGSLPLPSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 120
Db 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 120
QY 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 120
Db 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 120
QY 121 HVSGAVLTFGMSLYMVFQVTLISYQMPKHGKQVFWIRLLVWCVSALSMLTCSVL 180
Db 121 HVSGAVLTFGMSLYMVFQVTLISYQMPKHGKQVFWIRLLVWCVSALSMLTCSVL 180
QY 114 ----- 113
Db 114 ----- 113
QY 181 HSGNFGTDLQKHLWNPEDKGYLVHMTTAAEWSMSPFPGFLLTYRDPKISLRVEAN 240
Db 114 -----GYLVHMTTAAEWSMSPFPGFLLTYRDPKISLRVEAN 153
QY 241 LHGLTYLTAPCPINNERTLLSRD 265
Db 154 LHGLTYLTAPCPINNERTLLSRD 178

RESULT 7
Q61Q10 PRELIMINARY; PRT; 272 AA.
AC Q61Q10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Zgc:86754.
GN Name=zgc:86754;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

```

```

RA Klauner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC071426; AAH71426.1; -.
SQ SEQUENCE 272 AA; 30362 MW; B7FE8BDD89FC87FA CRC64;

Query Match 54.9%; Score 764.5; DB 2; Length 272;
Best Local Similarity 55.2%; Pred. No. 1.2e-55;
Matches 138; Conservative 48; Mismatches 63; Indels 1; Gaps 1;

QY 1 MWMFOGSLPLPSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWMFOGSLPLPSALVWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 119
Db 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 119
QY 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 119
Db 61 NIAAVLCIATYVRYKQVHALSP-BENVIKNKAGLVGLISCLGLSIVANFQKTLFAA 119
QY 120 HVSGAVLTFGMSLYMVFQVTLISYQMPKHGKQVFWIRLLVWCVSALSMLTCSVL 179
Db 120 HVSGAVLTFGMSLYMVFQVTLISYQMPKHGKQVFWIRLLVWCVSALSMLTCSVL 179
QY 121 HVSGAVLTFGMSLYMVFQVTLISYQMPKHGKQVFWIRLLVWCVSALSMLTCSVL 180
Db 121 HVSGAVLTFGMSLYMVFQVTLISYQMPKHGKQVFWIRLLVWCVSALSMLTCSVL 180
QY 180 HSGNFGTDLQKHLWNPEDKGYLVHMTTAAEWSMSPFPGFLLTYRDPKISLRVEAN 239
Db 180 HSGNFGTDLQKHLWNPEDKGYLVHMTTAAEWSMSPFPGFLLTYRDPKISLRVEAN 239
QY 181 MYSTLPGVEVKNKHLWTPGPGFTAHVSTISEMSLALSIFSFLLTYRDPKISLRVEAN 240
Db 181 MYSTLPGVEVKNKHLWTPGPGFTAHVSTISEMSLALSIFSFLLTYRDPKISLRVEAN 240
QY 240 NLHGLTYLT 249
Db 241 ELQSNHLYES 250

RESULT 8
AAH71426 PRELIMINARY; PRT; 272 AA.
AC AAH71426;
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

```

```

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071426; AAH71426.1; -.
KW Hypothetical protein.
SQ SEQUENCE 272 AA; 30362 MW; B7FE8BDD89FC87FA CRC64;

Query Match
Best Local Similarity 54.9%; Score 764.5; DB 2; Length 272;
Matches 138; Conservative 48; Mismatches 63; Indels 1; Gaps 1;

QY 1 MWNFQGLSFLPSALVVTWTAAGAFISFYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MWNFQGLCVLPVALVVTWTAATIFAYITAVLRHVDPLVPYISDTGTVAPEKCVGVML 60

QY 61 NIAAVLCIATIVYRYKOVHSLP-EENVIIKLNKAGVLGILSGISLVANFQKTLFA 119
DB 61 NVSAFLGVATVYRYKQLQALADVDDTRLNRLNVGVFGCCSFGMCVAVNFQKTLFS 120

QY 120 AHVSGAVLTGMSGLYMFVOTILSYOMQPKIHGQVFWIRLLIIVGCVSALSMLTCCSV 179
DB 121 MHLVGAILTFGICALYVFIQTALSYLMQPHHSKTFWIRLSVIGTSLISIMFVSVI 180

QY 180 LHSGNFTDLEOKLWNPEDKGVLMHTTAAEWSMSFSGFFGLFYIRDPQKISLRVEA 239
DB 181 MYTLPGEVNKKLWNPEDKGVLPDGPFGTAHVSTISEWSLSLSFISFLFYIRDFKKNLRSA 240

QY 240 NLHGLTYDT 249
DB 241 ELQSNHLYES 250

RESULT 9
Q8NBQ4 PRELIMINARY; PRT; 136 AA.
AC Q8NBQ4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018435; AAH18435.1; -.
DE InterPro; IPR000504; RNP_RNP_1; UNKNOWN 1.
DR InterPro; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 238 AA; 26253 MW; 51187567737F6C0 CRC64;

Query Match
Best Local Similarity 35.4%; Score 492.5; DB 2; Length 238;
Matches 97; Conservative 53; Mismatches 79; Indels 21; Gaps 3;

QY 1 MWNFQGLSFLPSALVVTWTAAGAFISFYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MLCFLGRMAFVPLLVWSSAAFIISYVAVLSGHVNPFLPYISDTGTTPSGIGFMI 60

QY 61 NIAAVLCIATIVYRYKOV-----HALSPENVIIKLNKAGVLGILSGISLVANFQ 113
DB 61 NFSAFLGAATWYTRYKIVQKQNTCYFSTFVFNLV-----SLVLGVGCFGMGIVANFQ 114

```

```

Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 131 MGSLYMFVOTILSYOMQPKIHGQVFWIRLLIIVGCVSALSMLTCCSVLHSGNFGTDLE 190
DB 1 MGSLYMFVOTILSYOMQPKIHGQVFWIRLLIIVGCVSALSMLTCCSVLHSGNFGTDLE 60

QY 191 OKLWNPEDKGVLMHTTAAEWSMSFSGFFGLFYIRDPQKISLRVEANLHGLTYDTA 250
DB 61 OKLWNPEDKGVLMHTTAAEWSMSFSGFFGLFYIRDPQKISLRVEANLHGLTYDTA 120

QY 251 PCPINNERTLLSRDI 266
DB 121 PCPINNERTLLSRDI 136

RESULT 10
Q8N682 PRELIMINARY; PRT; 238 AA.
AC Q8N682;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE FLJ11259 protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner B., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018435; AAH18435.1; -.
DE InterPro; IPR000504; RNP_RNP_1; UNKNOWN 1.
DR InterPro; PS00030; RRM_RNP_1; UNKNOWN 1.
SQ SEQUENCE 238 AA; 26253 MW; 51187567737F6C0 CRC64;

```

```
QY 114 KTTLPAAHVSGAVLTGEMGLYMFVQTLISYQMPKIHGKQVFIWIRLLLVINGVGSALSM 173
DB 115 ELAVPVVHDGALLAFVCGVYVTLQSLIISYKSCPQWNSLSTCHIRWISAVSCAAVPM 174
QY 174 LTCSSVLHSGNFGCTDLEQKLHWPEDKGYVLHMITTAAEWSMFSFGFPLTVIRDFQKI 233
DB 175 IVCASLISI-----TKLEWNPKEKDYIYHVVSICAIEWTVAFGFIFLTFIQDFQSV 226
QY 234 SLRVEANLH 243
DB 227 TLRISTEING 236

RESULT 11
Q9DC58 ID Q9DC58 PRELIMINARY; PRT; 238 AA.
AC Q9DC58;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200002N14 product:hypothetical RNA-binding region RNP-1 (RNA
DE recognition motif) containing protein, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 409:685-690 (2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akahiza S., Akimura T., Atai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004552; BAB23366.2; -
DR MGD; MGI:1918962; 1200002N14Rik.
DR InterPro; IPR000504; RNA_rec_mot.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26200 MW; AC89F1301B0A0048 CRC64;

Query Match 34.4%; Score 479.5; DB 2; Length 238;
Best Local Similarity 37.3%; Pred. No. 6.2e-32;
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;

QY 1 MWFQOGLSFLPSALVITSAAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
DB 1 MLCFLRGMFAVPFLLVWSSAAFIISYVAVLSGHVNPPLPYISDTGTPPGSGIFGMI 60
QY 61 NTAAVLCIATIVYRKQV-----HALSPENVIILKNAGLVGLISLGLSIVANFQ 113
DB 61 NFSAPLGAATMYTRYKIVEKQNETCVFSTPVENLV-----SLALGLVGCIGMIVANFQ 114
QY 114 KTTLPAAHVSGAVLTGEMGLYMFVQTLISYQMPKIHGKQVFIWIRLLLVINGVGSALSM 173
DB 115 ELAVPVVHDGALLAFVCGVYVTLQSLIISYKSCPQWNSLSTCHIRWISAVSCAAVPM 174
QY 174 LTCSSVLHSGNFGCTDLEQKLHWPEDKGYVLHMITTAAEWSMFSFGFPLTVIRDFQKI 233
DB 175 IVCASLISI-----TKLEWNPKEKDYIYHVVSICAIEWTVAFGFIFLTFIQDFQSV 226
QY 234 SLRVEANLH 242
DB 227 TLRISTEIN 235

RESULT 12
BAB23366 ID BAB23366 PRELIMINARY; PRT; 238 AA.
AC BAB23366;
DT 14-APR-2004 (TREMBlrel. 27, Created)
DT 14-APR-2004 (TREMBlrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBlrel. 27, Last annotation update)
DE Adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200002N14 product:hypothetical RNA-binding region RNP-1 (RNA
DE recognition motif) containing protein, full insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
```

```
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690(2001).
RP [3]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RP [4]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RP [5]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RP [6]
RC SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akabira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa Y., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004552; BAB23366.2; -
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26200 MW; AC89F1301B0A0048 CRC64;

Query Match 34.4%; Score 479.5; DB 2; Length 238;
Best Local Similarity 37.3%; Pred. No. 6.2e-32;
Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;

QY 1 MMWFOGSLFSLPVSALVITWTSAAFIYSITAVTLHHIDPALPYISDTGTVAPEKCLFGNML 60
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
1 MLCFLRGMAFVFPFLVWSSAFLISYVVVLSGVHNPFLPYISDTGTTPPESGIFGPMI 60

QY 61 NTAAVLCIATIVYRKQV-----HALSPENVIILNKAGLVGLSICLSIVANFQ 113
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
61 NFSAFIGAATWYTRYKIVEKQNETCYFSTPVENLV-----SLALGLVGCIGMIVANFQ 114

QY 114 KTTLFAAHVSGAVLTFGMGSLVMFVQTILSYQMOPKIHGKQVFWIRLLLVWCVGSALSM 173
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
115 ELAVFVHDGGALLAFVGVVYTLQSIISYKSCPQWNSLTTCVHRVAISAVSAAVYPM 174

QY 174 LTCSSVLSHNGFTDLEOKLHNPDKGYVLHMTTAAEWSMSPSFFGFFLTIRDFOKI 233
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
175 IACASLIS1-----TKLEWNPKEKDIYHVVSACEITWTVAGFFIFYFLTIDFQSV 226

QY 234 SURVEANLH 242
```

```
Db 227 TLR1STEIN 235
:::
:::

RESULT 13
QGNRS6
ID QGNRS6 PRELIMINARY; PRT; 287 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC431986 protein (Fragment).
GN Name=LOC431986;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RL Dev. Dyn. 225:384-391(2002).
RP [3]
RC SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070646; AAH70646.1; -
FT NON TER 1
SQ SEQUENCE 287 AA; 31871 MW; 5E9814FA48BE462 CRC64;

Query Match 33.9%; Score 471.5; DB 2; Length 287;
Best Local Similarity 38.0%; Pred. No. 3.5e-31;
Matches 93; Conservative 56; Mismatches 79; Indels 17; Gaps 4;

QY 3 WFOQGLSFLPVSALVITWTSAAFIYSITAVTLHHIDPALPYISDTGTVAPEKCLFGMUNI 62
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
52 WCLQGAFLPVSILVWSSAGFLFSLISVLIGHVFPFVYISDTGTTPPESGVFGFMISV 111

QY 63 AAVLCIATIVYRKQVHALSPENVIILNKAGLVGLSICLSIVANFQKTL 117
Db |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
112 SAMLGAAATWYTRY-----MILSRQNLSDIFLPYFNKISLAIGLFGCIGMIVATFQEMAV 167

QY 118 FAHVSGAVLTFGMGSLVMFVQTILSYQMOPKIHGKQVFWIRLLLVWCVGSALSMUTCS 177
```



```
Db 168 PAVHDAGALITFCGMYLLQSYISKSCPTWNTNTRATCHIRMTVSLIAFIAVVPMSVFS 227
QY 178 SVLHSGNFGTDLQKHLWNPEDKGYVLLHMTTAAEWSMSPFPFGLTIRDFOKISLRV 237
Db 228 --ILSG-----RKRLDWKPSDEGYPHLTSAICETWVAFGNMYFLTIRDFQGVSIQI 279
QY 238 EANLH 242
Db 280 STEIH 284

RESULT 14
AAH70646
ID AAH70646 PRELIMINARY; PRT; 287 AA.
AC AAH70646;
DT 13-MAY-2004 (TrEMBLrel. 27, Created)
DT 13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT 13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallos J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Klein S., Strauberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC070646; AAH70646.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 287 AA; 31871 MW; 5E9814FA488BE462 CRC64;
```

```
Query Match 33.9%; Score 471.5; DB 2; Length 287;
Best Local Similarity 38.0%; Pred. No. 3.5e-31;
Matches 93; Conservative 56; Mismatches 79; Indels 17; Gaps 4;

QY 3 WFOQGLSPLSALVIVTSAAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI 62
```

```
Db 52 MCLOGAALPSILVIVSSAGFLFSYIISVLIGHVPPFPFYISDTGTSPSPESGVFGFMISV 111
QY 63 AAVLCIATYVRYKQVHALSPENVIK-----LNKAGLVGLSCGLSIVANFOKTL 117
Db 112 SANLGAATWTRY----MILRQNLISIDPLPIYFNKISLAIGLFGCIGMIVATFQEMAV 167
QY 118 FAAHVSGLVLTFGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCS 177
Db 168 PAVHDAGALITFCGMYLLQSYISKSCPTWNTNTRATCHIRMTVSLIAFIAVVPMSVFS 227
QY 178 SVLHSGNFGTDLQKHLWNPEDKGYVLLHMTTAAEWSMSPFPFGLTIRDFOKISLRV 237
Db 228 --ILSG-----RKRLDWKPSDEGYPHLTSAICETWVAFGNMYFLTIRDFQGVSIQI 279
QY 238 EANLH 242
Db 280 STEIH 284

RESULT 15
O8QGB2
ID O8QGB2 PRELIMINARY; PRT; 238 AA.
AC O8QGB2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE VHSV-induced protein-6.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22129223; PubMed=12134009;
RA O'Farrell C., Vaghefi N., Cantonnet M., Buteau B., Boudinot P.,
RA Benmansour A.;
RT "Survey of transcript expression in rainbow trout leukocytes reveals a
RT major contribution of interferon-responsive genes in the early
RT response to a rhadovirus infection.";
RL J. Virol. 76:8040-8049(2002).
DR EMBL; AF483532; AAM18471.1; -.
SQ SEQUENCE 238 AA; 26650 MW; 06BEDE247670D134 CRC64;

Query Match 31.6%; Score 439.5; DB 2; Length 238;
Best Local Similarity 40.3%; Pred. No. 1.3e-28;
Matches 96; Conservative 45; Mismatches 88; Indels 9; Gaps 4;

QY 1 MWFOQGLSPLSALVIVTSAAFIPSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MLWFMGICFLPISLVINSSSTFIVSYLIALPEHDVDVIFPYISDTGAEPSPSCVFLMT 60
QY 61 NTAAVLCIATYVRYKQVHALSPER-NVILKLNKAGLVGLSCGLSIVANFOKTLPA 119
Db 61 VITAPAGMATMYARYKPKVEKLNKAGGVRRPSLNQAFAWIGMLSCGLMCFVATFOETTTA 120
QY 120 AHVSGAVLTFCGMSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCSV 179
Db 121 VHDAGAILFFVSGVDYTLIQSIISYKAPF--YGCSLALCR----VRTGMATFAFLAVPFT 174
QY 180 LHSNGNFGTDLQKHLWNPEDKGYVLLHMTTAAEWSMSPFPFGLTIRDFOKISLRV 237
Db 175 VVCAIFVT--QTTLRKTEDEDNVHLVSASEMIVAFSFLIPFFTYIHLKFKTLKL 230

Search completed: January 4, 2005, 12:20:11
Job time : 192 secs
```

THIS PAGE BLANK (USPTO)